

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 10:59:20 ; Search time 59.03 Seconds
(without alignments)
90.849 Million cell updates/sec

Title: US-09-785-059-3

Perfect score: 176
Sequence: 1 RMIRVQRCRAIRHWRIRIQGLRRLRVV 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94	53.4	858	15	071974 human immun
2	92	52.3	872	15	091U21 human immun
3	92	52.3	872	15	091U20 human immun
4	90	51.1	856	15	077694 human immun
5	90	51.1	856	15	091U25 human immun
6	90	51.1	859	15	092937 human immun
7	90	51.1	859	15	092937 human immun
8	89	50.6	853	15	056563 human immun
9	89	50.6	854	15	056319 human immun
10	89	50.6	856	15	092877 simian-huma
11	89	50.6	856	15	074599 human immun
12	89	50.6	856	15	041539 human immun
13	89	50.6	856	15	0905M7 human immun
14	89	50.6	856	15	0902G3 human immun
15	89	50.6	859	15	P87924 human immun
16	89	50.6	861	15	091U24 human immun

17	89	50.6	866	15	Q73301 human immun
18	88	50.0	357	15	Q78100 human immun
19	88	50.0	358	15	Q78141 human immun
20	88	50.0	852	15	089797 human immun
21	88	50.0	854	15	092762 human immun
22	88	50.0	855	15	Q74841 human immun
23	88	50.0	858	15	092874 human immun
24	88	50.0	869	15	Q73302 human immun
25	87	49.4	853	15	056108 human immun
26	87	49.4	860	15	09DH01 human immun
27	87	49.4	860	15	09E534 human immun
28	87	49.4	860	15	09E518 human immun
29	87	49.4	861	15	09E527 human immun
30	87	49.4	861	15	09E523 human immun
31	87	49.4	862	15	093024 human immun
32	85	48.3	358	15	Q78140 human immun
33	85	48.3	854	15	056566 human immun
34	85	48.3	862	15	09DVL5 human immun
35	84	47.7	849	15	09PEX5 human immun
36	84	47.7	852	15	041883 human immun
37	84	47.7	852	15	041885 human immun
38	84	47.7	853	15	Q73372 human immun
39	84	47.7	861	15	Q99414 human immun
40	83	47.2	136	15	Q79566 human immun
41	83	47.2	854	15	Q97016 human immun
42	83	47.2	855	15	Q902H5 human immun
43	83	47.2	859	15	Q72940 human immun
44	83	47.2	860	15	Q9WB56 human immun
45	83	47.2	860	15	Q72984 human immun

ALIGNMENTS

RESULT 1
ID 071974 PRELIMINARY: PRT: 858 AA.
AC 071974;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ENVELOPE GLYCOPROTEIN.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
NC NCBL_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HIV-1NC;
RA MEDLINE=98440562; PubMed=9765443;
RX Mwaengo D.M., Novembre F.J.;
RT "Molecular cloning and characterization of viruses isolated from
RT chimpanzees with pathogenic human immunodeficiency virus type 1
RT infections";
RL J. VIROL. 72:8976-8987(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-HIV-1NC;
RA Mwaengo D.M., Novembre F.J.;
RT Submitted (FEB-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF049495; AAC68857.1; -;
DR InterPro; IPR000328; Env-GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 858 AA; 97704 MW; 6FD2AB63400A5BF9 CRC64;

Query Match 53.4%; Score 94; DB 15; Length 858;
Best Local Similarity 75.0%; Pred. No. 0.00044;
Matches 21; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1 RWIRVQRCRAIRHIMRIRROGLRRML 28
| | | | | | | | | | | | | | | | | |
DB 830 RIEVVQRCRAIRHIMRIRROGLRRML 857

RESULT 2

OY1U21 PRELIMINARY: PRT: 872 AA.

AC OY1U21: 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
GN GP160.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_Taxid=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PE131;

RA Daniels R.S., Beddows S., Wilson P., Douglas N.W., Patel D.,
Ives K.J., Easterbrook P., Weber J.N.;

RT "An association between amino acid substitutions in the 'Silent Face'
of human immunodeficiency virus type 1 gp120 and resistance to
RT antibody mediated neutralization.";

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

EMBL: AJ286339; CAB86150.1; -

InterPro: IPR000328; Env.GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00517; GP120; 1.

KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.

SEQUENCE 872 AA; 98941 MW; FE9B28B0FF1CD3C8 CRC64;

Query Match 52.3%; Score 92; DB 15; Length 872;

Best Local Similarity 75.0%; Pred. No. 0.0008; Mismatches 7; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 RWIRVQRCRAIRHIMRIRROGLRRML 28
| | | | | | | | | | | | | | | | | |
DB 844 RIEVVQRCRAIRHIMRIRROGLRRML 871

RESULT 3

OY1U20 PRELIMINARY: PRT: 872 AA.

AC OY1U20: 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
GN GP160.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_Taxid=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PE131;

RA Daniels R.S., Beddows S., Wilson P., Douglas N.W., Patel D.,
Ives K.J., Easterbrook P., Weber J.N.;

RT "An association between amino acid substitutions in the 'Silent Face'
of human immunodeficiency virus type 1 gp120 and resistance to
RT antibody mediated neutralization.";

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

EMBL: AJ286340; CAB86151.1; -

InterPro: IPR000328; Env.GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00517; GP120; 1.

KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.

SEQUENCE 872 AA; 99032 MW; D89C0CDD06A3E1F04 CRC64;

Query Match 52.3%; Score 92; DB 15; Length 872;
Best Local Similarity 75.0%; Pred. No. 0.0008; Mismatches 7; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 RWIRVQRCRAIRHIMRIRROGLRRML 28
| | | | | | | | | | | | | | | | | |
DB 844 RIEVVQRCRAIRHIMRIRROGLRRML 871

RESULT 4

OY1U25 PRELIMINARY: PRT: 856 AA.

AC OY1U25: 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
GN ENV. POLYPEPTIDE.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_Taxid=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CAMBRIDGE;

RA McIntosh A.A., Karpas A.;

RT "Nucleotide sequence of a Cambridge isolate of human immunodeficiency
virus type 1.";

RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.

EMBL: D10112; BAA00998.1; -

InterPro: IPR000328; Env.GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00517; GP120; 1.

KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.

SEQUENCE 856 AA; 97493 MW; 19D32F205A94410D CRC64;

Query Match 51.1%; Score 90; DB 15; Length 856;

Best Local Similarity 75.0%; Pred. No. 0.0014; Mismatches 7; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 RWIRVQRCRAIRHIMRIRROGLRRML 28
| | | | | | | | | | | | | | | | | |
DB 828 RIEVVQRCRAIRHIMRIRROGLRRML 855

RESULT 5

OY1U25 PRELIMINARY: PRT: 858 AA.

AC OY1U25: 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
GN GP160.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_Taxid=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PE106;

RA Daniels R.S., Beddows S., Wilson P., Douglas N.W., Patel D.,
Ives K.J., Easterbrook P., Weber J.N.;

RT "An association between amino acid substitutions in the 'Silent Face'
of human immunodeficiency virus type 1 gp120 and resistance to
RT antibody mediated neutralization.";

EMBL: AJ286335; CAB86146.1; -

InterPro: IPR000328; Env.GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00517; GP120; 1.

KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.

SEQUENCE 858 AA; 99032 MW; D89C0CDD06A3E1F04 CRC64;


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RP SEQUENCE FROM N.A.
RC STRAIN-SHIV-89.6;
RX MEDLINE=96186751; PubMed=8627800;
RA Reimann K.A., Li J.T., Voss G., Lekutis C., Tenner-Racz K., Racz P.,
RA Lin W., Montefiori D.C., Lee-Parritz D.E., Lu Y., Collman R.G.,
RA Sodroski J., Letvin N.L.;
RT "An env gene derived from a primary human immunodeficiency virus type
RT 1 isolate confers high in vivo replicative capacity to a chimeric
RT simian/human immunodeficiency virus in rhesus monkeys.";
RL J. Virol. 70:3198-3206(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SHIV-89.6;
RA Reimann K.A., Li J.T., Voss G., Lekutis C., Tenner-Racz K., Racz P.,
RA Lin W., Montefiori D.C., Lee-Parritz D.E., Lu Y., Collman R.G.,
RA Sodroski J., Letvin N.L.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF038398; AAB99966.1; -.
DR InterPro: IPR000328; Env.GP41.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 854 AA; 97265 MW; 72A4B131DCE4F7 CRC64;

Query Match 50.6%; Score 89; DB 15; Length 854;
Best Local Similarity 75.0%; Pred. No. 0.0019; Mismatches 7; Indels 0; Gaps 0;
Matches 21; Conservative 0;

Oy 1 RWIRVQRCRAIRHIRIRIGLRRL 28
Db 826 RVIEVQACRAIRHIRIRIGLERIL 853

RESULT 10
Oy 092877 PRELIMINARY; PRT; 856 AA.
AC 092877;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ENVELOPE GLYCOPROTEIN.
GN ENV.
OS Simian-Human immunodeficiency virus.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=57667;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9098984; PubMed=9882298;
RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B.A., Hofmann W.,
RA Steenbeke J., Halloran M., Fanton J.W., Axthelm M.K., Letvin N.L.,
RA Sodroski J.G.;
RT "Changes in human immunodeficiency virus type 1 envelope glycoproteins
RT responsible for the pathogenicity of a multiply passaged simian-human
RT immunodeficiency virus (SHIV-HXB2).";
RL J. Virol. 73:976-984(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B., Hofmann W.,
RA Halloran M., Axthelm M.W., Letvin N.L., Sodroski J.G.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF041850; AAD12142.1; -.
DR InterPro: IPR000328; Env.GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 856 AA; 97151 MW; C50BE0388FB73659 CRC64;

Query Match 50.6%; Score 89; DB 15; Length 856;
Best Local Similarity 75.0%; Pred. No. 0.0019; Mismatches 7; Indels 0; Gaps 0;
Matches 21; Conservative 0;

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Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 RWIRVQRCRAIRHIRIRIGLRRL 28
Db 828 RVIEVQACRAIRHIRIRIGLERIL 855

RESULT 11
Oy 074599 PRELIMINARY; PRT; 856 AA.
AC 074599;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ENV.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MCK1;
RX MEDLINE=90101366; PubMed=1688473;
RA Cloyd M.W., Moore B.E.;
RT "Spectrum of Biological Properties of Human Immunodeficiency Virus
RT (HIV-1) Isolates.";
RL Virology 174:103-116(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-MCK1;
RA Iwattani Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; D86068; BAA12995.1; -.
DR InterPro: IPR000328; Env.GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 856 AA; 97287 MW; 238042A234C5685 CRC64;

Query Match 50.6%; Score 89; DB 15; Length 856;
Best Local Similarity 75.0%; Pred. No. 0.0019; Mismatches 7; Indels 0; Gaps 0;
Matches 21; Conservative 0;

Oy 1 RWIRVQRCRAIRHIRIRIGLRRL 28
Db 828 RVIEVQACRAIRHIRIRIGLERIL 855

RESULT 12
Oy 041539 PRELIMINARY; PRT; 856 AA.
AC 041539;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C10;
RX MEDLINE=98105804; PubMed=9445059;
RA Connor R.I., Korber B.T.M., Graham B.S., Hahn B.H., Ho D.D.,
RA Walker B.D., Neumann A.U., Vernund S.H., Westecky J., Jackson S.,
RA Fenamore E., Cao Y., Gao F., Kalam S., Kunstman K.J., McDonald D.,
RA McWilliams N., Trkola A., Moore J.P., Wolinsky S.M.;
RT "Immunological and virological analyses of persons infected by human
RT immunodeficiency virus type 1 while participating in trials of
RT recombinant gp120 subunit vaccines.";

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